

EXHIBIT 13

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch:

☐ Use Mega BLAST Strand option

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
DYGNSTYESTDLETRALSSQPMISISEASDNLKRSDDMDFSGLNVFHYGWQLWSDGWAAITV
DPEPASSATITDPKKANRFHRTLTLTLWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNS
AELTPSDHFPWGTGGGLGMVYQEPRENHPGFHMRSSGYFAGMIAGQTHTFSLKFSQTYT
KLNERYAKNNVSSKNYSQGEMLFSLQEGFLLAKLVGLYSYGDHNCHEFTQGENLTSQGT
FRSQTMGGAVFFDLPMKPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINV
LVPIGVKGSFMNATQRPQAWTVLAYQPVLRYQELEIATQLLASKGIWFGSGSPSSRHAMS
YKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF.
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
msqknksafmqpvvnvsadlaaivgagpmprteiikkmdyikenslqdpnkrninpddkl
akvfgtekipidmfqmtkmvsqhiik
```

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Align**

Sequence 1 lcl|seq_1 Length 955 *PMPE PTA-2462*

Sequence 2 lcl|seq_2 Length 86 *Probst SEQ ID NO: 5*

No significant similarity was found

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using **BLAST** engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in **BLASTN** program only:

Reward for a match: Penalty for a mismatch:

☒ Use Mega BLAST Strand option

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
DTGNSPTIESTDLTHALSSQPMLSISEASDNQLRSDDMDFSGLNVPHYGWQGLWSGWAKTQ
DPEPASSATITDPKKANRFHRTLTLTWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNS
AELTPSDHPFWGITGGGLGMMVYQEPRENHPGFHMRSSGYFAGMIAGQTHTFSLKFSQTYT
KLNERYAKNNVSSKNYSQGEMLFSLQEGFLLAKLVGLYSYGDHNCHHFYTQGENLTSQGT
FRSQTMGGAVFFDLPMKPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINV
LVPIGVKGSFMNATQRPQAWTVELAYQPVLRYQELEIATQLLASKGIWFGSGSPSSRHAMS
YKISQQTQPLSWLTLHFQYHGFYSSSTFCNVYNGEIALRF.
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
ivgagpmprteikkmdwyikenslqdpntkrninpddklakvfgtekipdmfgmtkmvsq
```

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Align**

Sequence 1 lcl|seq_1 Length 955 *PMPE ATCC PTA-2462*

Sequence 2 lcl|seq_2 Length 61 *Probst SEQ ID NO: 6*

N significant similarity was found

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using **BLAST** engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in **BLASTN** program only:

Reward for a match: Penalty for a mismatch:

☐ Use **Mega BLAST** Strand option

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
DTGNSPTESITDITRALSSQFMLSISEASUNQLKRSDDMDFGULNVPHIGWQGLWSWGWAQIQ
DPEPASSATITDPKANKRPHRTLTLTLWLPAGYVPSFKHRSPLIANTLWGNMLLATESLKNS
AELTPSDHPPFWGITGGGLGMMVYQEPRENHPGFHMRSSGYFAGMIAGQTHTFSLKFSQTYT
KLNERYAKNNVSSKNYSCQGEMLFSLQEGFLLAKLVGLYSYGDHNCCHFYTOGENLTSQGT
FRSQTMGGAVFFDLPMKPFGSTHILTAPFLGALGIYSSLSHFTVEGAYPRSFSTKTPLINV
LVPIGVKGSFMNATQRPQAWTVELAYQPVLRYRQELEIATQLLASKGIWFGSGSPSSRHAMS
YKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF.
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
aatscelanqhghlqfplltrslmlmlpsqsqshr
```

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: gap extension: x_dropoff: expect: wordsize: Filter ☒ **Align**Sequence 1 lc|seq_1 Length 955 *PMPE ATCC PTA-2462*Sequence 2 lc|seq_2 Length 36 *Probst SEQ ID NO: 7*

No significant similarity was found

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch:

☐ Use Mega BLAST Strand option

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
DTGNSFTSTLTLRALSSQFTLSISEASUNQLRSDDMLFSGNLVPHIGWQQLWSGWAKTY  
DPEPASSATTIDPKKANRFHRTLTLTWPAGYVPSPKHRSPLIANTLWGNMLLATESLKNS  
AELTPSDHPFWGITGGGLGMMVYQEPRENHPGFHMRSSGYFAGMIAGQTHTFSLKFSQTYT  
KLNERYAKNNVSSKNYSCQGEMLFSLQEGFLAKLVGLYSYGDHNCCHFYTQGENLTSQGT  
FRSQTMGGAVFFDLPMKPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINV  
LVPIGVKGSFMNATQRPQAWTVLAYQPVLRYQELEIATQLLASKGIWFGSGSPSSRHAMS  
YKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF.
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
lrhhaslqtnmdisnfpf
```

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Align**

Sequence 1 lcl|seq_1 Length 955 *PMPE ATCC BTA-2462*

Sequence 2 lcl|seq_2 Length 18 *PROBST SEQ ID NO: 8*

No significant similarity was found

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using **BLAST** engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)
Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch:

☐ Use Mega BLAST Strand option

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
DTGNSPTIESYULTRALSSQFMLSISEASUNQLRSDUMDFSGLNVPHTGWQGLWSGWAKTQ
DPEPASSATITDPKKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNS
AELTPSDHPFWGITGGGLMMVYQEPRENHPGFHMRSSGYFAGMIAGQTHTFSLKFSQTYT
KLNERYAKNNVSSKNYSCQGEMLFSLQEGFLLAKLVGLYSYGDHNCHEFYTQGENLTSQGT
FRSQTMGGAVFFDLPMKPGFSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINV
LVPIGVKGSFMINATQRPQAWTVELAYQPVLRYQELEIATQLLASKGIWFGSGSPSSRHAMS
YKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF.
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

lalwn

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Align**

Sequence 1 lc|seq_1 Length 955 *PMPG ATCC PTA-2462*

Sequence 2 lc|seq_2 Length 5 *Probst SEQ ID NO: 9*

No significant similarity was found

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch:

☐ Use Mega BLAST Strand option

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
DYGNSTFESTDLTRALSSQFTLSISEASUNQLRSDDMFSGLNVPHTGWAGLWSGWAKTV
DPEPASSATITDPKCANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNS
AELTPSDHPPFWGITGGGLGMMVYQEPRENHPGFHMRSSGYFAGMIAGQTHTFSLKFSQTYT
KLNERYAKNNVSSKNYSQGEMLFSLQEGFLLAKLVGLYSYGDHNCHEFYTQGENLTSQGT
FRSQTMGGAFFDLPMPKPGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINV
LVPIGVKGSFMNATQRPQAWTVLAYQPVLYRQELEIATQLLASKGIWFGSGSPSSRHAMS
YKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF.
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
ccyrvnhhid
```

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Align**

Sequence 1 lcl|seq_1 Length 955 **6 PMPE ATCC PTA-2462**

Sequence 2 lcl|seq_2 Length 11 **PROBST SEQ ID NO: 10**

No significant similarity was found

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch:

☒ Use Mega BLAST Strand option

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
DTGNSPTESDULTRALSSQFRLSISEASDNQLRSDDMDFSGLNVPHYGWQGLWSGWAKTV  
DPEPASSATITDPKKANRPHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMILLATESLKNS  
AELTPSDHPFWGITGGGLGMMVYQEPRENHPGFHMRSSGYFAGMIAGQTHTFSLKFSQTYT  
KLNERYAKNNVSSKNYSCQGEMLFSLQEGFLLAKLVGLYSYGDHNCHEFYTQGENLTSQGT  
FRSQTMGGAVFFDLPMKFFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINV  
LVPIGVKGSFMNATQRPQAWTVELAYQPVLVYRQELEIATQLLASKGIWFGSGSPSSRHAMS  
YKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF.
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
vdviidsvaalvpkselegeigdvhvglqarmmsq
```

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ Align

Sequence 1 lcl|seq_1 Length 955

PMPE ATCC PTA-2462

Sequence 2 lcl|seq_2 Length 36

Probst SEQ ID NO: 11

No significant similarity was found

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch:

☐ Use Mega BLAST Strand option

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
DIGNSPTIESTDLTRALSSQPMLSISEASDNQLKRSDDMDFSGLNVPHYIGWQLWSWGWAQY  
DPEPASSATTIDPKKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMILLATESLKNS  
AELTPSDHFPWGITGGGLGMMVYQEPRENHPGFHMRSSGYFAGMIAGQTHTFSLKFSQTYT  
KLNERYAKNNVSSKNYSCQGEMLFSLQEGFLAKLVGLYSYGDHNCHEFYTQGENLTSQGT  
FRSQTMGGAVFFDLPMKPPGSTHILTAPFLGALGIYSSLSHFTVEGAYPRSFSTKTPLINV  
LVPIGVKGSFMNATQRPQAWTVLAYQPVLYRQELEIATQLLASKGIWFGSGSPSSRHAMS  
YKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF.
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
mpriigidipakkkkisltyigigpalskeiiaarlqlnpearaaglteeevgrlnallqs  
dyvvegdlrrrvqsdkrlitihayrgqrhrslpvrgrtktnsrtrkgkrktiagkkk
```

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Align**

Sequence 1 lcl|seq_1 Length 955

Sequence 2 lcl|seq_2 Length 121

No significant similarity was found

PMDE ATCC PTA-2462
Prubst SEQ ID NO: 12

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using **BLAST** engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in **BLASTN** program only:

Reward for a match: Penalty for a mismatch:

☐ Use **Mega BLAST** Strand option

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
DTGNSPYESTDLTHALSSQPMLSISEASUNQLRSDDMFSGELNVFRTGWQGLWSGWAKTV
DPEPASSATITDPKKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNS
AELTPSDHPPFWGITGGGLGMMVYQEPRENHPCGFHMRSSGYFAGMIAGQTHTFSLKFSQTYT
KLNERYAKNNVSSKNYSCQGEMLFSLQEGFLLAKLVGLYSYGDHNCCHFYTQGENLTSQGT
FRSQTMGGAVFFDLPMKPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINV
LVPIGVKGSFMNATORPQAWTVELAYQPVLRYQELEIATQLLASKGIWFGSGSPSSRHAMS
YKISQQTQPLSWLTLHFQYHGFISSSTFCNYLNGEIALRF.
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
rptnkrninpddklakvfgt
```

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Align**

Sequence 1 lcl|seq_1 Length 955 *PMPE ATCC PTA-2462*

Sequence 2 lcl|seq_2 Length 20 *Probst SEQ ID NO: 13*

No significant similarity was found

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch:

☐ Use Mega BLAST Strand option

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
DTGNSPTIESTDLTHALSSQPMLSISEASLNLQKRSDDMDFSGLNVFHYGWQGLWSGWAKTV
DPEPASSATITDPKKNRFRHTLLLTLWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNS
AELTPSDHPFWGITGGGLGMMVYQEPRENHHPGFHMRSSGYFAGMIAGQTHTFSLKFSQTYT
KLNERYAKNNVSSKNYSCQGEMLFSLQEGFLAKLVGLYSYGDHNCCHFYTQGENLTSQGT
FRSQTMGGAVFFDLPMKFFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINV
LVPIGVKGSFMNATQRPQAWTVLAYQPVLRYQELEIATQLLASKGIWFGSGSPSSRHAMS
YKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF.
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
ddklakvfgtekipdmfamt
```

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Align**

Sequence 1 lcl|seq_1 Length 955 *PMPE ATLC PTA-2462*

Sequence 2 lcl|seq_2 Length 20 *Probst SEQ ID NO:14*

No significant similarity was found